

RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

09/821819

Source:

OIPE

Date Processed by STIC:

10/05/01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/821819

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPINA" HEADERS, WHICH WERE INSERTED BY PTO

- 1 Wrapped Nucleics
 Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length
The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering
The numbering under each 5* amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length.
Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence
<210> sequence id number
<400> sequence id number
000
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 9 Use of n's or Xaa's
 (NEW RULES)
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 10 Invalid <213>
 Response
- 11 Use of <220>
Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH - Biotechnology Systems Branch - 08/21/2001

The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

OIPF

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/821,819

DATE: 10/05/2001
TIME: 09:36:36

Input Set : A:\37174-7.ST25.txt
Output Set: N:\CRF3\10052001\I821819.raw

3 <110> APPLICANT: Tsao, Desiree
4 Telliez, Jean-Baptiste
5 McDonagh, Thomas
6 Lin, Lih-Ling
7 Hsu, Sang
8 Xu, Guang-Yi
9 Malakian, A. Karl
11 <120> TITLE OF INVENTION: N-TRADD ACTIVE SITE AND USES THEREOF
13 <130> FILE REFERENCE: 37174/7
15 <140> CURRENT APPLICATION NUMBER: US 09/821,819
C--> 17 <141> CURRENT FILING DATE: 2001-09-13
19 <150> PRIOR APPLICATION NUMBER: US 60/195,370
21 <151> PRIOR FILING DATE: 2000-04-06
23 <160> NUMBER OF SEQ ID NOS: 6
25 <170> SOFTWARE: PatentIn version 3.0
27 <210> SEQ ID NO: 1
29 <211> LENGTH: 168
31 <212> TYPE: PRT
33 <213> ORGANISM: Homo sapiens
35 <400> SEQUENCE: 1
37 Met Ala Ala Gly Gln Asn Gly His Glu Trp Val Gly Ser Ala Tyr Leu
38 1 5 10 15
40 Phe Val Glu Ser Ser Leu Asp Lys Val Val Leu Ser Asp Ala Tyr Ala
41 20 25 30
43 His Pro Gln Gln Lys Val Ala Val Tyr Arg Ala Leu Gln Ala Ala Leu
44 35 40 45
46 Ala Glu Ser Gly Gly Ser Pro Asp Val Leu Gln Met Leu Lys Ile His
47 50 55 60
49 Arg Ser Asp Pro Gln Leu Ile Val Gln Leu Arg Phe Cys Gly Arg Gln
50 65 70 75 80
52 Pro Cys Gly Arg Phe Leu Arg Ala Tyr Arg Glu Gly Ala Leu Arg Ala
53 85 90 95
55 Ala Leu Gln Arg Ser Leu Ala Ala Ala Leu Ala Gln His Ser Val Pro
56 100 105 110
58 Leu Gln Leu Glu Leu Arg Ala Gly Ala Glu Arg Leu Asp Ala Leu Leu
59 115 120 125
61 Ala Asp Glu Glu Arg Cys Leu Ser Cys Ile Leu Ala Gln Gln Pro Asp
62 130 135 140
64 Arg Leu Arg Asp Glu Glu Leu Ala Glu Leu Glu Asp Ala Leu Arg Asn
65 145 150 155 160
67 Leu Lys Cys Gly Ser Gly Ala Arg
68 165
71 <210> SEQ ID NO: 2
73 <211> LENGTH: 13
75 <212> TYPE: PRT
C--> 77 <213> ORGANISM: Artificial/Unknown
79 <220> FEATURE:

Does Not Comply
Corrected Data Needed

The type of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

Errored: 213 response may not be
duplications. Appropriate response are
either "Artificial Sequence", "Unknown" or
the name of some species.

RAW SEQUENCE LISTING
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Input Set : A:\37174-7.ST25.txt
Output Set: N:\CRF3\10052001\I821819.raw

```

81 <221> NAME/KEY: PEPTIDE
83 <222> LOCATION: (1)..(13)
85 <223> OTHER INFORMATION: CD40 peptide synthesized using Fmoc solid-phase methods
87 <400> SEQUENCE: 2
89 Ser Asn Thr Ala Pro Val Gln Glu Thr Leu His Gly
90 1 5 10
93 <210> SEQ ID NO: 3
95 <211> LENGTH: 6
97 <212> TYPE: PRT
C--> 99 <213> ORGANISM: Artificial/Unknown
101 <220> FEATURE:
103 <221> NAME/KEY: peptide
105 <222> LOCATION: (1)..(6)
107 <223> OTHER INFORMATION: shortest CD40 sequence recognized by TRAF2
109 <400> SEQUENCE: 3
111 Tyr Pro Ile Gln Glu Thr
112 1 5
115 <210> SEQ ID NO: 4
117 <211> LENGTH: 9
119 <212> TYPE: PRT
C--> 121 <213> ORGANISM: Artificial/Unknown
123 <220> FEATURE:
125 <221> NAME/KEY: peptide
127 <222> LOCATION: (1)..(9)
129 <223> OTHER INFORMATION: C-TRAF2 consensus sequence
131 <400> SEQUENCE: 4
133 Gln Val Pro Phe Ser Lys Glu Glu Cys
134 1 5
137 <210> SEQ ID NO: 5
139 <211> LENGTH: 4
141 <212> TYPE: PRT
C--> 143 <213> ORGANISM: Artificial/Unknown
145 <220> FEATURE:
147 <221> NAME/KEY: peptide
149 <222> LOCATION: (1)..(4)
151 <223> OTHER INFORMATION: TNFR2 sequence motif; X may be any amino acid
153 <400> SEQUENCE: 5
W--> 155 Ser Xaa Xaa Glu
156 1
159 <210> SEQ ID NO: 6
161 <211> LENGTH: 5
163 <212> TYPE: PRT
C--> 165 <213> ORGANISM: Artificial/Unknown
167 <220> FEATURE:
169 <221> NAME/KEY: peptide
171 <222> LOCATION: (1)..(5)
173 <223> OTHER INFORMATION: CD40 sequence motif; X may be any amino acid
175 <400> SEQUENCE: 6
W--> 177 Pro Xaa Gln Xaa Thr

```

Errors: Responses may not be duplications

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The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

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DATE: 10/05/2001

PATENT APPLICATION: US/09/821,819

TIME: 09:36:36

Input Set : A:\37174-7.ST25.txt

Output Set: N:\CRF3\10052001\I821819.raw

178 1

5

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/821,819

DATE: 10/05/2001

TIME: 09:36:37

Input Set : A:\37174-7.ST25.txt

Output Set: N:\CRF3\10052001\I821819.raw

L:17 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:77 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:2
L:99 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3
L:121 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4
L:143 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5
L:155 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:165 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:6
L:177 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6